

Figure 1A

Query = C54D2.5 CE02562 CALCIUM CHANNEL ALPHA-1 SUBUNIT LG:6
Database: Non-redundant Database of GenBank EST Division
824,500 sequences; 302,742,428 total letters.

H55225 CHR220164 Homo sapiens genomic clone C22_207 5'.
Length = 168

Plus Strand HSPs:

Score = 136 (63.8 bits), Expect = 2.5e-10, P = 2.5e-10
Identities = 23/31 (74%), Positives = 29/31 (93%), Frame = +1

Query: 440 VISLEGWTDIMYYVQDAHSFNNWIYFVLLIV 470 *Seq ID NO. 24*
VI LEGW IMYYV DAHSF N IYF LLI
Sbjct: 1 VITLEGWVEIMYYVMDAHSFYNFYIFILLII 93 *Seq ID NO. 25*

H55617 CHR220556 Homo sapiens genomic clone C22_757 5'.
Length = 98

Plus Strand HSPs:

Score = 102 (47.9 bits), Expect = 2.8e-05, P = 2.8e-05
Identities = 19/23 (82%), Positives = 23/23 (100%), Frame = +2

Query: 243 NINLTAIRTVRVLRLRAVNRIP 265 *Seq ID NO. 26*
NINL AIRTVRVLRLPL A NR P
Sbjct: 29 NINLSAIRTVRVLRLKAINRVP 97 *Seq ID NO. 27*

H55223 CHR220162 Homo sapiens genomic clone C22_204 5'.
Length = 94

Plus Strand HSPs:

Score = 87 (40.8 bits), Expect = 0.0039, P = 0.0039
Identities = 14/19 (73%), Positives = 18/19 (94%), Frame = +2

Query: 154 MAVIMINCVTLGMYRPCED 172 *Seq ID NO. 28*
M VI NCVTLGMY PC D
Sbjct: 2 MLVILLNCVTLGMYQPCDD 58 *Seq ID NO. 29*

Figure 1B

H55544 CHR220483 Homo sapiens genomic clone C22_651 5'.

Length = 123

Plus Strand HSPs:

Score = 65 (30.5 bits), Expect = 3.8, P = 0.98

Identities = 12/23 (52%), Positives = 18/23 (78%), Frame = +1

Query: 246 LTAIRTVRVLRPLRAVNRIPSMR 268

RT R LRPLRA R MR

Sbjct: 55 IKSLRTLRLALRPLRALSRLFEGMR 123

Seq ID NO. 30
Seq ID NO. 31

F07776| HSC2HD061 H. sapiens partial cDNA sequence; clone c-2hd06

Length = 343

Plus Strand HSPs:

Score = 100 (46.9 bits), Expect = 0.00057, P = 0.00057

Identities = 21/41 (51%), Positives = 31/41 (75%), Frame = +3

Query: 1480 PTIIRVMRVLRIARVLKLLKMAKGIRSLDDTVGEALPQVGN 1520

PT+ RV+R+ RI R+L+L+K AKGIR+LL + +LP + N

Sbjct: 57 PTLXRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFN 179

Seq ID NO. 32
Seq ID NO. 33